REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated February 24, 2003, the period for response to which will expire on May 24, 2003.

Claims 1-4 and 30-37 are under consideration in this application. Claims 35-36 are being amended based upon page 22, lines 9-11, as set forth above and in the attached marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention. Pages 34-36 are being amended to be consistent therein and with the drawings and other portions of the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due reconsideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Informality Objections & Rejections

Claims 1-4 and 30-37 were rejected under 35 U.S.C. § 112, first paragraph, for new matters including (1) that one primer pair is designed for each exon; (2) that the corresponding primer pairs are designed simultaneously; and (3) a means for implementing such a design.

Applicants respectfully contend that there were no matters since the alleged new matters are supported by the specification as explained in details as follows. Regarding (1) of the new matter issues, one primer pair is designed for each exon according to the invention. For example, the Embodiment 1 of the invention designs four primer pairs for four exons and one primer pair for each exon ("the partial sequences given in SEQ ID NOS: 5 and 6 were extracted form exon 1 (SEQ ID: 1), ...", see page 33, line 13-20). Further more, on pages 21-22 and Fig. 4, a forward primer A4 and a reverse primer A5 are designed for the exon A3 .

Regarding (2), the Pattern III of the invention deigns corresponding primers for a plurality of exons simultaneously (pages 35-36; Table 1, col. 1, row 1 "simultaneously treated by p process (here, 50), parallel and distributed"). As indicated, the relevant recitation is revised into "simultaneously treated by 50 parallel processes," which is fully supported by the description of the Embodiment 2 (pages 33-36). The invention generates 5000 primers per day via Patterns I-III by using parallel and distributed computers (page 36, last paragraph). The output of 5000

primers per day is approximately 100 times faster than a traditional manual system. It takes about 5 minutes for an experienced scientist to design one primer based upon existing primer design software. Assuming the scientist works 8 hours (480 minutes) per day, the scientist designs only 50 primer pairs per day (480/5 = 96 primers ~ about 100 primers = 50 primer pairs).

In particular, the output of 5000 primers per day was contributed by three simultaneously processing steps in the Patterns I-III. According to Table 1, the primer design time T3 (page 36, lines 6-7) required to design 1000 primers (1st col. 5th row of Table 1) was 49.8 minutes. The 49.8 minutes was reduced to 1.0 minute by approximately 50 parallel primer designing processes on 50 exons simultaneously in Pattern I.

In Table 1, the exon screening time T2 (page 36, lines 4-5) required to generate 1000 primers (1st col. 5th row of Table 1) was 598.2 minutes. The 598.2 minutes was reduced to 12 minute (13.0 –1.0 = 12) by approximately 50 parallel exon screening processes in Pattern II.

In Table 1, the exon prediction time T1 (page 36, lines 3-4) required to generate 1000 primers (1st col. 5th row of Table 1) was 1244.8 minutes. The 1244.8 minutes was reduced to 24.9 minute (37.9 –13.0 = 24.9) by approximately 50 parallel exon prediction processes on 50 DNAs in Pattern III.

Regarding (3), the means for simultaneously designing corresponding primers for a plurality of exons are parallel and distributed computers (page 36, last paragraph) installed with "primer design software"(page 35, line 20).

Claims 35-36 were rejected under 35 U.S.C. § 112, second paragraph, for reciting a trademark designation instead of an element, function or step. As indicated, claims 35-36 have been amended as required by the Examiner.

Accordingly, the withdrawal of the outstanding informality rejections is in order, and is therefore respectfully solicited.

Prior Art Rejection

The 35 U.S.C. § 103(a) rejections have been withdrawn.

In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art references upon which the rejections in the Office Action rely, Applicants respectfully contend that the prior art references cannot anticipate the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application as amended is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

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Marked-up Version of Amended Claims

35. A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer by conducting [BLAST] homology searches for a full sequence of the primer via at least one repeat database and at least one genome database.

36. A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer by conducting a [BLAST] homology search for any undesirable sequence contained therein.

Marked-up Copy of Specification

running the necessary programs was used for each of the patterns.

fix the typo

Pttern I

Only primer designing was carried out. Pattern I involved running a process for ~~extracting~~ designing a pair of partial sequences from ~~the predetermined template DNA~~ a predicted and screened partial sequence ~~A1~~ based on primer design software corresponding to the partial sequence ~~extraction~~ selection processor ~~403~~ 409,410. The partial sequence ~~extraction~~ selection conditions were as follows.

(1) base length: 20 to 28 bps;

(2) GC content: 50 to 60%;

(3) Tm: 50 to 80°C; |Tm|: below 20°C; and

(4) located as close as possible to the 5' end or 3' end.

Pattern II

For pattern II, exons were screened, and primers were then designed. For pattern II, exons were screened based on selected conditions from previously prepared exon database 307, ~~template DNA~~ a predicted sequence ~~A1~~ was transferred ~~through the input 401~~ to a partial sequence ~~extraction~~ screening processor ~~403~~, and the process for ~~extracting~~ selecting partial sequences was run based on primer design software corresponding to the partial sequence ~~extraction~~ selection processor ~~403~~ 409,410. The exon screening conditions are given

below. The partial sequence ~~extraction~~ selection conditions were the same as for pattern I.

(1) exon length: 300 bps or less

(2) exons predicted by an exon predicting program

(3) found in EST database, and expression confirmed

(4) unknown function (not found in protein database)

(5) SNP potential (variation in EST database)

Pattern III

After the exon prediction, exons were screened, and primers were then designed. For pattern III, exons were predicted using software corresponding to the exon predicting program 304 from genomic DNA sequences 303, the output exon sequences 305 were compiled into a database 307 through a sequence input interface 306, exons were screened in the exon database 307 on the basis of the set conditions, the template DNA sequence A1 was transferred through the input 401 to the partial sequence extraction processor 403,. and the process for ~~extracting~~ selection partial sequences was run by primer design software corresponding to the partial sequence ~~extraction~~ selection processors ~~403~~ 409, 410. The exon screening conditions were the same as for pattern II. The partial sequence ~~extraction~~ selection conditions were the same as for pattern I.

Table 1 shows the results of calculations for the time needed to run patterns I through III one thousand times, respectively. In Table 1, "T1" represents the time (minutes) needed for exon prediction, "T2" represents the time (minutes) needed for exon screening, and "T3" represents the time (minutes) needed for primer design.

Table 1

	I	II	III
T1 (min)	0	0	1244.8
T2 (min)	0	598.2	598.2
T3 (min)	49.8	49.8	49.8
Calculated time (min) needed to design 1000 primers	49.8	648 (10.8 H)	1892.8 (31.55 H)
When simultaneously treated by R processes (here, 50) by parallel and distributed computers	1.0	13.0	37.9

The results of Table 1 show that the primer design system of the present invention can be used to design about 5000 sets of primers per day through parallel and distributed computers, which means about 150,000 primers could be sufficiently prepared a year.